

## Application

mRNA Sequencing from high-quality inputs

**Unlock the Potential of Every Sample**



# Application:

## mRNA Sequencing from high-quality input

### Application Challenges

- Next-generation sequencing of mRNA (mRNA-Seq) provides a comprehensive view of the **coding** transcriptome. To ensure optimal sequencing economy, effective enrichment of mRNA molecules prior to library construction is required.
- Enrichment for mRNA with oligo-dT bead technology relies on **intact, poly-adenylated** transcripts, and may result in a bias toward the 3'-portions of transcripts if input RNA is not of a high quality.
- Library construction workflows for mRNA-Seq comprise four stages: mRNA enrichment, cDNA synthesis, adapter ligation and library amplification. These **laborious, multi-step protocols are often difficult to complete in a single workday**.
- Many of the enzymatic and bead-based steps involved in mRNA-Seq library prep are **inherently inefficient and biased**, leading to the loss of low-abundance and "difficult" (e.g., GC-rich) transcripts.
- For most RNA-Seq applications it is important to retain **RNA strand orientation information**.
- Analysis and visualization of RNA-Seq data requires **advanced bioinformatics skills**.

### Roche Sample Prep Workflow



Data on file.

\*Automation and Connectivity solutions are in development.

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## Solutions



The **KAPA mRNA HyperPrep Kit** offers a complete mRNA library preparation solution from a wide range of inputs. Kits include **KAPA Pure Beads** for efficient, tunable reaction cleanups, and **KAPA HiFi HotStart ReadyMix** for high-efficiency, low-bias library amplification.

**KAPA Adapters** are QC-tested for NGS performance and barcode cross-contamination.



**KAPA Library Quantification Kits** enable accurate, qPCR-based library quantification. Compatible with Roche LightCycler® 96 and LightCycler® 480 real-time PCR systems.



Qualified, single-click **Genialis™** data analysis pipeline and visualization tools.

## Benefits

- Prepare high-quality libraries in a **single workday** with a **streamlined, automation-friendly** mRNA capture and library preparation workflow.
- Achieve **optimal sequencing economy** with effective mRNA enrichment and highly efficient library construction; which limits the number of reads associated with unwanted content and PCR duplicates.
- **Introduce minimal bias** during library amplification with KAPA HiFi HotStart ReadyMix to better preserve **GC-rich** and **low-abundance** transcripts.
- **Achieve >99% strandedness** to more accurately identify antisense transcripts and demarcate the boundaries of closely situated or overlapping genes.
- **Take control of your data** with the intuitive, cloud-based Genialis software\*, which offers pre-configured pipelines and real-time visualization tools for biologists with limited bioinformatics expertise.
- Enjoy greater peace of mind with **integrated support** for a complete mRNA-Seq workflow solution.



 **Unlock the Potential of Every Sample**

# Unlock the Potential of Every Sample

As the first step in the NGS workflow continuum, sample prep holds the key to unlocking the potential of every sample. Because NGS samples are precious, the best methods are needed to process more samples successfully, obtain more information from every sample, and optimize your sequencing resources. From sample collection to sequencing-ready libraries, Roche Sample Prep Solutions offer workflows for different sample types and sequencing applications that are **proven**, **simple** and **complete**.



## Infographic

RNA-Seq made simple, from input to analysis. Roche Sequencing Solutions, 2018.



## Webinar

The power of RNA: Broad application of RNA-based sequencing for transcriptome and genome analysis, featuring Dr. John Puritz (Department of Biological Sciences, University of Rhode Island, Kingston) and Heather Geiger (New York Genome Center, New York). Presented by Science and Roche Sequencing Solutions, 4 September 2018.



## Publications

Guo M. et al. EZH2 Represses the B Cell Transcriptional Program and Regulates Antibody-Secreting Cell Metabolism and Antibody Production. *J. Immunol.* 2018;200(3):1039. doi:10.4049/jimmunol.1701470.

Nakamura BN, et al. A20 regulates canonical wnt-signalling through an interaction with RIPK4. *PLoS ONE.* 2018;13(5):e0195893. doi:10.1371/journal.pone.0195893.

Albariño CG, et al. Transcriptional analysis of viral mRNAs reveals common transcription patterns in cells infected by five different filoviruses. *PLoS ONE.* 2018;13(8):e0201827. doi:10.1371/journal.pone.0201827.

## Ordering information

Roche Cat. No.	KAPA Code	Description	Pack Size
08098115702	KK8580	KAPA mRNA HyperPrep Kit	24 reactions
08098123702	KK8581	KAPA mRNA HyperPrep Kit	96 reactions
08278555702	KK8722	KAPA Dual-Indexed Adapter Kit (15 µM)	96 x 20 µL
07960140001	KK4824	KAPA Library Quantification Kit (Illumina®/Universal)	500 reactions
07960298001	KK4854	KAPA Library Quantification Kit (Illumina/LC480)	500 reactions

Published by:

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MC--00949 04/2022